

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Pastan, Ira
Chang, Kai

(ii) TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
Present on Mesothelium, Mesotheliomas and Ovarian Cancers
and Methods and Kits for Targeting the Antigen

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: San Francisco
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Not yet assigned
(B) FILING DATE: Not yet assigned
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/776,271
(B) FILING DATE: 01-DEC-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/US97/00224
(B) FILING DATE: 03-JAN-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/010,166
(B) FILING DATE: 05-JAN-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Faris, Susan K.
(B) REGISTRATION NUMBER: 41,739
(C) REFERENCE/DOCKET NUMBER: 015280-259110US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 576-0200
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 100..1986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTC CCG AGG GGG GCT CCC GAG CGA CAG CGG CTG CTG CCT GCG GCT CTG Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu Leu Pro Ala Ala Leu 150 155 160 165	594
GCC TGC TGG GGT GTG CGG GGG TCT CTG CTG AGC GAG GCT GAT GTG CGG Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser Glu Ala Asp Val Arg 170 175 180	642
GCT CTG GGA GGC CTG GCT TGC GAC CTG CCT GGG CGC TTT GTG GCC GAG Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly Arg Phe Val Ala Glu 185 190 195	690
TCG GCC GAA GTG CTG CTA CCC CGG CTG GTG AGC TGC CCG GGA CCC CTG Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser Cys Pro Gly Pro Leu 200 205 210	738
GAC CAG GAC CAG CAG GAG GCA GCC AGG GCG GCT CTG CAG GGC GGG GGA Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala Leu Gln Gly Gly Gly 215 220 225	786
CCC CCC TAC GGC CCC CCG TCG ACA TGG TCT GTC TCC ACG ATG GAC GCT Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val Ser Thr Met Asp Ala 230 235 240 245	834
CTG CGG GGC CTG CTG CCC GTG CTG GGC CAG CCC ATC ATC CGC AGC ATC Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro Ile Ile Arg Ser Ile 250 255 260	882
CCG CAG GGC ATC GTG GCC GCG TGG CGG CAA CGC TCC TCT CGG GAC CCA Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg Ser Ser Arg Asp Pro 265 270 275	930
TCC TGG CGG CAG CCT GAA CGG ACC ATC CTC CGG CCG CGG TTC CGG CGG Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg Pro Arg Phe Arg Arg 280 285 290	978
GAA GTG GAG AAG ACA GCC TGT CCT TCA GGC AAG AAG GCC CGC GAG ATA Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys Lys Ala Arg Glu Ile 295 300 305	1026
GAC GAG AGC CTC ATC TTC TAC AAG AAG TGG GAG CTG GAA GCC TGC GTG Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu Leu Glu Ala Cys Val 310 315 320 325	1074
GAT GCG GCC CTG CTG GCC ACC CAG ATG GAC CGC GTG AAC GCC ATC CCC Asp Ala Ala Leu Ala Thr Gln Met Asp Arg Val Asn Ala Ile Pro 330 335 340	1122
TTC ACC TAC GAG CAG CTG GAC GTC CTA AAG CAT AAA CTG GAT GAG CTC Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His Lys Leu Asp Glu Leu 345 350 355	1170
TAC CCA CAA GGT TAC CCC GAG TCT GTG ATC CAG CAC CTG GGC TAC CTC Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln His Leu Gly Tyr Leu 360 365 370	1218
TTC CTC AAG ATG AGC CCT GAG GAC ATT CGC AAG TGG AAT GTG ACG TCC Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys Trp Asn Val Thr Ser 375 380 385	1266

CTG GAG ACC CTG AAG GCT TTG CTT GAA GTC GAC AAA GGG CAC GAA ATG Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp Lys Gly His Glu Met 390 395 400 405	1314
AGT CCT CAG GCT CCT CGG CGG CCC CTC CCA CAG GTG GCC ACC CTG ATC Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln Val Ala Thr Leu Ile 410 415 420	1362
GAC CGC TTT GTG AAG GGA AGG GGC CAG CTA GAC AAA GAC ACC CTA GAC Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp Lys Asp Thr Leu Asp 425 430 435	1410
ACC CTG ACC GCC TTC TAC CCT GGG TAC CTG TGC TCC CTC AGC CCC GAG Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys Ser Leu Ser Pro Glu 440 445 450	1458
GAG CTG AGC TCC GTG CCC CCC AGC AGC ATC TGG GCG GTC AGG CCC CAG Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp Ala Val Arg Pro Gln 455 460 465	1506
GAC CTG GAC ACG TGT GAC CCA AGG CAG CTG GAC GTC CTC TAT CCC AAG Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys 470 475 480 485	1554
GCC CGC CTT GCT TTC CAG AAC ATG AAC GGG TCC GAA TAC TTC GTG AAG Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys 490 495 500	1602
ATC CAG TCC TTC CTG GGT GGG GCC CCC ACG GAG GAT TTG AAG GCG CTC Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu 505 510 515	1650
AGT CAG CAG AAT GTG AGC ATG GAC TTG GCC ACG TTC ATG AAG CTG CGG Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg 520 525 530	1698
ACG GAT GCG GTG CTG CCG TTG ACT GTG GCT GAG GTG CAG AAA CTT CTG Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu 535 540 545	1746
GGA CCC CAC GTG GAG GGC CTG AAG GCG GAG GAG CGG CAC CGC CCG GTG Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val 550 555 560 565	1794
CGG GAC TGG ATC CTA CGG CAG CGG CAG GAC GAC CTG GAC ACG CTG GGG Arg Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly 570 575 580	1842
CTG GGG CTA CAG GGC GGC ATC CCC AAC GGC TAC CTG GTC CTA GAC CTC Leu Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu 585 590 595	1890
AGC GTG CAA GAG ACC CTC TCG GGG ACG CCC TGC CTC CTA GGA CCT GGA Ser Val Gln Glu Thr Leu Ser Gly Thr Pro Cys Leu Leu Gly Pro Gly 600 605 610	1938
CCT GTT CTC ACC GTC CTG GCA CTG CTC CTA GCC TCC ACC CTG GCC Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala Ser Thr Leu Ala 615 620 625	1983
TGAGGGCCCC ACTCCCTTGC TGGCCCCAGC CCTGCTGGGG ATCCCCGCCT GGCCAGGAGC	2043

AGGCACGGGT GATCCCCGTT CCACCCCAAG AGAACTCGCG CTCAGTAAAC GGGAACATGC	2103
CCCCTGCAGA CAAAAAAA AAAAAAAA AAAAA	2138

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Leu Gln Arg Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro			
1	5	10	15

Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala		
20	25	30

Arg Thr Leu Ala Gly Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly		
35	40	45

Val Leu Thr Thr Pro His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu		
50	55	60

Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val			
65	70	75	80

Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr		
85	90	95

Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp		
100	105	110

Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala		
115	120	125

Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys		
130	135	140

Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu			
145	150	155	160

Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser		
165	170	175

Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly		
180	185	190

Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser		
195	200	205

Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala		
210	215	220

Leu Gln Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val			
225	230	235	240

Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro
 245 250 255
 Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg
 260 265 270
 Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg
 275 280 285
 Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys
 290 295 300
 Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu
 305 310 315 320
 Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met Asp Arg
 325 330 335
 Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His
 340 345 350
 Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln
 355 360 365
 His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys
 370 375 380
 Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp
 385 390 395 400
 Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln
 405 410 415
 Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp
 420 425 430
 Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys
 435 440 445
 Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp
 450 455 460
 Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp
 465 470 475 480
 Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser
 485 490 495
 Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu
 500 505 510
 Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr
 515 520 525
 Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu
 530 535 540
 Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu
 545 550 555 560

Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp
 565 570 575

Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr
 580 585 590

Leu Val Leu Asp Leu Ser Val Gln Glu Thr Leu Ser Gly Thr Pro Cys
 595 600 605

Leu Leu Gly Pro Gly Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala
 610 615 620

Ser Thr Leu Ala
 625

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Gly Gly Gly Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Glu Asp Leu Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Glu Asp Leu
1

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Pro Arg Phe Arg Arg
1 5